Amendments to the Specification

1. Please amend the title by replacing the title on page 1, line 1, with the following title:

MULTIPLE DISPLACEMENT AMPLIFICATION

2. Please delete the paragraph on page 23, line 3, that reads in its entirety: "[##THE FOLLOWING PARAGRAPH IS NEW##]".

3. Please delete the paragraph on page 35, line 15, that reads in its entirety: "[##THE FOLLOWING PARAGRAPH IS NEW##]".

4. Please delete the paragraph on page 47, line 28, that reads in its entirety: "@@**".

5. Please replace the paragraph bridging pages 10 and 11 with the following paragraph:

The target sequence, which is the object of amplification, can be any nucleic acid. The target sequence can include multiple nucleic acid molecules, such as in the case of whole genome amplification, multiple sites in a nucleic acid molecule, or a single region of a nucleic acid molecule. For multiple strand displacement amplification, generally the target sequence is a single region in a nucleic acid molecule or nucleic acid sample. For whole genome amplification, the target sequence is the entire genome or nucleic acid sample. A target sequence can be in any nucleic acid sample of interest. The source, identity, and preparation of many such nucleic acid samples are known. It is preferred that nucleic acid samples known or identified for use in amplification or detection methods be used for the method described herein. The nucleic acid sample can be, for example, a nucleic acid sample from one or more cells, tissue, or bodily fluids such as blood, urine, semen, lymphatic fluid, cerebrospinal fluid, or amniotic fluid, or other biological samples, such as tissue culture cells, buccal swabs, mouthwash, stool, tissues slices, biopsy aspiration, and archeological samples such as bone or mummified tissue. Types of useful target samples include blood samples, urine samples, semen samples, lymphatic fluid samples, cerebrospinal fluid samples, amniotic fluid samples, biopsy samples, needle aspiration

biopsy samples, cancer samples, tumor samples, tissue samples, cell samples, cell lysate samples, ~~acrude cell lysate samples~~crude cell lysate samples, forensic samples, archeological samples, infection samples, nosocomial infection samples, production samples, drug preparation samples, biological molecule production samples, protein preparation samples, lipid preparation samples, ~~ans/or carbohydrate~~and/or carbohydrate preparation samples.

6. Please replace the paragraph bridging pages 38 and 39 with the following paragraph:

Denaturation of nucleic acid molecules to be amplified is common in amplification techniques. This is especially true when amplifying genomic DNA. In particular, PCR uses multiple denaturation cycles. Denaturation is generally used to make nucleic acid strands accessible to primers. It was discovered that the target nucleic acids, genomic DNA, for example, need not be ~~denatured* for efficient~~denatured for efficient multiple displacement amplification. It was also discovered that elimination of a denaturation step and denaturation conditions has additional advantages such as reducing sequence bias in the amplified products. In preferred forms of the disclosed method, the nucleic acid sample or template nucleic acid is not subjected to denaturating conditions and/or no denaturation step is used. In some forms of the disclosed method, the nucleic acid sample or template nucleic acid is not subjected to heat denaturating conditions and/or no heat denaturation step is used. It should be understood that while sample preparation (for example, cell lysis and processing of cell extracts) may involve conditions that might be considered denaturing (for example, treatment with alkali), the denaturation conditions or step eliminated in some forms of the disclosed method refers to denaturation steps or conditions intended and used to make nucleic acid strands accessible to primers. Such denaturation is commonly a heat denaturation, but can also be other forms of denaturation such as chemical denaturation. It should be understood that in the disclosed method where the nucleic acid sample or template nucleic acid is not subjected to denaturing conditions, the template strands are accessible to the primers (since amplification occurs). However, the template stands are not made accessible via general denaturation of the sample or template nucleic acids.

7. Please amend the title by replacing the title on page 107, line 1, with the following title:

MULTIPLE DISPLACEMENT AMPLIFICATION